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(without alignments)
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                                                                                                               December 6, 2002, 23:36:56; Search time 52 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  350425 seqs, 194966369 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_NA:*
                                                                      OM nucleic - nucleic search, using sw model
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Listing first 45 summaries
                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1525
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                                                                                                                                                                                                                                   Sequence:
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1: /cgn2\_6/ptcdata/1/pubpna/USO7\_PUBCOMB.seq:\*
2: /cgn2\_6/ptcdata/1/pubpna/PCT\_NEW\_PUB.seq:\*
3: /cgn2\_6/ptcdata/1/pubpna/USO6\_NEW\_PUB.seq:\*
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5: /cgn2\_6/ptcdata/1/pubpna/USO7\_NEW\_PUB.seq:\*
6: /cgn2\_6/ptcdata/1/pubpna/USO8\_NEW\_PUB.seq:\*
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14: /cgn2\_6/ptcdata/1/pubpna/USO8\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Constitution of the consti	Sequence 13, Appl	Source 343, App	Sociones 144, App							٠.	٠.		Sequence 12287, A	Sequence 10531, A	Sequence 14649. A		2	Sequence Z, Appli	sednence 3, Appli	Sequence 5191, Ap
SUMMARIES	qı	US-09-782-378A-13	US-09-964-824A-545	US-09-964-824A-544	US-09-765-231A-19	US-09-964-824A-582	US-09-954-456-1089	US-09-865-812-1	US-09-880-107-2090	115-09-917-8004-1421	IS-00-880-107-0057	US-09-755-665-13	TE-00-017-000%-120E	15:00:01:00:00:00:00:00:00:00:00:00:00:00:	05-09-900-352-1228/	US-09-960-352-10531	US-09-960-352-14649	US-09-960-352-7066	US-09-912-628-2	115-09-912-628-3	20 00 000 000	US-09-960-352-5191
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| 132 | TTAGCTCATCAAAGTAATTCTATTTTAGTCCTGTTTCTATTGCCACTGCT | 191 | 192 | 194 | 194 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 | 195 |

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Sequence 7567, Sequence 409, As Sequence 409, As Sequence 409, Sequence 1792, Sequence 1792, Sequence 1792, Sequence 1792, Sequence 1793, Sequence 2321, Sequence 1748, Sequence 1	n 1345; Ls 0; Gaps	ACCAAGACCAT 71              TCAGGATCAC 143  GTATAGACAA 131           ATACCGCCAG 203
20 124.2 8.1 388 10 US-09-660-352-7567 22 123.2 8.1 439 10 US-09-960-352-10330 23 123 8.1 2089 9 US-09-992-598-409 24 123 8.1 2089 9 US-09-992-598-409 25 123 8.1 2089 10 US-09-992-534-09 26 123 8.1 2089 10 US-09-992-534-09 27 123 8.1 2089 10 US-09-992-734-09 28 123 8.1 2089 10 US-09-992-734-09 30 123 8.1 2089 10 US-09-997-442-09 31 123 8.1 2089 10 US-09-997-442-09 32 123 8.1 2089 10 US-09-997-442-09 33 123 8.1 2089 10 US-09-991-153-409 34 123 8.1 2089 10 US-09-991-153-409 35 123 8.1 2089 10 US-09-991-153-409 36 121.8 8.0 12089 10 US-09-991-153-409 37 120 7.9 421 10 US-09-991-153-12468 41 115.8 7.6 445 10 US-09-960-352-1314 44 113 7.4 403 10 US-09-960-352-11740 44 113 7.4 403 10 US-09-960-352-11740 44 113 7.4 403 10 US-09-960-352-11740 45 113 7.4 403 10 US-09-960-352-11740 46 113 7.4 403 10 US-09-960-352-11740 47 113 7.4 403 10 US-09-960-352-11740 48 113 7.4 403 10 US-09-960-352-11740 49 113 7.4 403 10 US-09-960-352-11740 40 US-09-980-442-09 41 113 7.4 403 10 US-09-960-352-11740 42 114 8 7.5 398 10 US-09-960-352-11740 44 113 7.4 403 10 US-09-960-352-11740 45 113 7.4 403 10 US-09-960-352-11740 46 113 7.4 403 10 US-09-960-352-11740 47 US-08-08-08-08-08-08-08-08-08-08-08-08-08-	ch 28.7%; Score 437; DB 10; Length 1 Similarity 60.6%; Pred. No. 6e-101; 716; Conservative 0; Mismatches 465; Indels	GAGACCCTCAAGGCGACGCGCTCAAAAACCGACACCAGTCATCACGACCAAGACCAT
20 124. 21 123. 22 123. 23 124. 24 122. 25 125. 26 125. 27 127. 28 122. 29 122. 29 122. 30 123. 31 112. 32 121. 33 118. 34 122. 34 122. 35 121. 36 121. 37 121. 38 118. 39 118. 39 118. 39 118. 39 118. 39 118. 39 118. 39 118. 39 118. 31 117. 30 118. 31 117. 31 117. 44 115. 45 117. 46 115. 47 117. 48 117. 48 117. 49 115. 40 115. 41 115. 42 117. 44 115. 44 115. 45 117. 46 117. 47 117. 48 117. 49 117. 40 117	Query Ma Best Loc Matches	Oy 12 G Db 84 G Oy 72 C Db 144 C

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us-10-025-514-15.rnpb

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APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1092 CCACCAGAAGTTAAATTTAATAAACCATTCGTTTTTCTGATGATCGAGCAGAACACTAAA 1151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1164 CCCCCAGAGGTCAAGTTCAACAAACCCTTTGTCTTTAATGATTGAACAAAATACCAAG 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAG 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         792 CAACATTTAGAGAATGAGTTGACTCATGACATTATTACTAAATTTTTAGAGAACGAGGAT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         864 CAGCACCIGGAAAAIGAACICACCCACGAIAICAICACCAAGIICCIGGAAAAIGAAGAC 923
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                                                                                                                                                                                                                                                                                                                                                                                                                   624 GITITIGCICTIGGIGAATIACATCITCTTIAAAGGCAAAIGGGAGAGACCTTITGAAGIC 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                           671
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                                                                                                                                                                                      444 AGCGAGGGCCTGAAGCTAGTGGATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCA 503
                                                                                                                                                                                                                            432 GAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAAATTAATGATTAT 491
                                                                                                                                                                                                                                                  564 GIGGAGAAGGGIACICAAGGGAAAAIIGIGGAIIIIGGICAAGGAGCIIGACAGAGACACA 623
                                                                                                                                                                                                                                                                                                                                                                               552 GICITCGCACTAGITAACTAIATITITTTCAAGGGTAAGTGGGAACGTCCTITCGAGGTT 611
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                                                                           312 AGAACTTTGAATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTG 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 ITCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 Trigcaariecrereceregeaceaaceaacereacacacaaaarecregaaceere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 AACITIAAITIGACCGAAATCCCAGAAGCCCAAATICACGAGGGTTITCAAGAGTIGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.1%; Score 429; DB 10; Length 1352; 60.2%; Pred. No. 6.3e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 470;
TITLE OF INVENTION: Sets
FILE REFERENCE: 688290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR PELING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US/60/236,028 PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(1352)
; OTHER INFORMATION: n=a,t,g or c
US-09-964-824A-545
                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.28
Matches 711; Conservative
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                         SEQ ID NO 545
LENGTH: 1352
                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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171 CCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTCGCCTTCAGCCTATACCGCCAG 230
                                               291 TITGCAATGCTCTCCCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTG 350
                                                                                                                                                                             951 AGAAGGTCTGCCAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAAG 1010
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                                                                                           192 ITCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTA 251
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                                                                                                                                                          252 AACTITAAITTGACCGAAATCCCAGAAGCCCAAATTCACGAGGGTTTTCAAGAGTTGTG 311
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                                                                                                                                                                                                                                                                                      372 ICTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAACTATATCATAGT 431
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 932 AGAAGGICIGCCAGCITACATITACCCAAACIGICCATIACIGGAACCIAIGAICIGAAG 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1152 AGCCCATTGTTATGGGTAAGGTTGTCAACCCAACTCAGAA 1192
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; Patent No. US20020102531A1
; GENERAL INFORMATION:
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OTHER INFORMATION: n=a, t, g or c
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US-09-964-824A-544
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1251 TCTCCCCTCTTCATGGGAAAGTGGTGAATCCCACCCAAAA 1291

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APPLICANT: Searle/Monsanto
APPLICANT: Phippard, Deborah
APPLICANT: Vasanthakamur, Geetha
APPLICANT: Vasanthakamur, Geetha
APPLICANT: Dotson, Stanton
APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
TITLE OF INVENTION: vectors, and cells
FILE REFRENCE: SO-321 PR
CURRENT APPLICATION NUMBER: US/09/765,231A
CURRENT FILING DATE: 2001-01-18
NUMBER OF SEQ ID NOS: 82
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                                                                                                                                                                                                                                                                                                                                                                  Length 1390;
                                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 407; DB 10; Length 139 60.1%; Pred. No. 2.3e-93; tive 0; Mismatches 470; Indels
     Sequence 19, Application US/09765231A Patent No. US20020119452A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               Matches 711; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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US-09-765-231A-19
                                                                                                                                                                                                                                                                       SEQ ID NO 19
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Sequence 582, Application US/09964824A

Sequence 582, Application US/09964824A

Patent No. US20020102531A1

PATENT NO. US20020102531A1

APPLICANT: Horrigan, Stephen

TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-73

CURRENT APPLICATION NUMBER: US/09/964,824A

CURRENT PILING DATE: 2001-09-27

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236,033

PRIOR FILING DATE: 2000-09-28

PRIOR PILING DATE: 2000-09-28

PRIOR PILING DATE: 2000-09-28

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PRIOR PILING DATE: 2000-09-28

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                                                                                                                                        790 TICAACATITAGAGAATGAGTIGACTCATGACATTATTACTAAATTTTTAGAGAACGAGG 849
731 ATTAATGAAGTA-TTTAGGTAACGCTACTGCTATTTTTTTTTACCAGACGAAGGTAAGC 789
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80.7%; Pred. No. 5.1e-47;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 582
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Matches 260; Conservative
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1437 GAAATGGACGGTCAATGTAAGAGAGACTTGAAGTGTTGTATGGGTATGTGGGTAAGTCC 1496
                  1197 ICCGGAAAGTCTTTCAAGGCCGGTGTTTGTCCACCAAAGAAGTCCGCTCAATGTTTGAGA 1256
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                                                                                                                            134 GAGATGGATGGCCAGTGCAAGGTGACTTGAAGTGTTGCATGGGCATGTGTGGGAAATCC 393
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APPLICANT: Rastell1, Luca
APPLICANT: Smithson, Glennda
TITLE OF INVENTION: Method of Detecting inflammatory Lung Disorders
TITLE OF INVENTION: Method of Detecting inflammatory Lung Disorders
CURRENT APPLICATION NUMBER: US/09/865,812
CURRENT FILING DATE: 2001-05-28
RIOR APPLICATION NUMBER: 60/207,104
PRIOR PILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
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80.7%; Pred. No. 5.1e-47;
tive 0; Mismatches 62; Indels 0;
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APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO
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Patent No. US20020142981A1
GENERAL INFORMATION:
                                                                                                                                                                                        1497 TGTGTTTCCCCAGTCAAGGCCT 1518
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; Patent No. US20020115626A1
; GENERAL INFORMATION:
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LENGTH: 594
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1317 GACACTIGIGIATCAAGIGICIAGACCCAGITGACACCCCAAACCCAACTAGAAGAAG 1376
                                                                                           1437 GAAATGGACGGTCAATGTAAGAGACTTGAAGTGTTGTATGGGTATGTGTGGGTAAGTCC 1496
                          1197 TCCGGAAAGTCTTTCAAGGCCGGTGTTTGTCCACCAAAGAAGTCCGCTCAATGTTTGAGA 1256
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CURRENT FILING DATE: 2001-09-18
PRIOR PELICATION NUMBER: US/60/233,617
PRIOR PELICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-25
PRIOR PELICATION NUMBER: US/60/234,923
PRIOR PELING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR PELING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-26
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PELING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
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; Patent No. US20020115057A1
; GENERAL INFORMATION:
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US-09-954-456-1989
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LENGTH: 594
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PRIOR FILING DATE: 2001-06-13
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NUMBER OF SEQ ID NOS: 1740
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14.4%; Score 219.8; DB 10; Length 1422;
Best Local Similarity 50.0%; Pred. No. 4.2e-46;
Matches 548; Conservative 0; Mismatches 547; Indels 0;
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CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 1422
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ORGANISM: Homo sapiens
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69 ACCIGICATITGCCCCAACAAAAIGCCACICICIAIAAGAIGCCAICIAICAAIGCIGAI 128
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                                                             129 TTTGCCTTCAGGCTGTATCGGAAGCTCTCTGGGAGAACCCAGATTTGAACATCTTCTTC 188
                                                                                                168 AGTCCTGTTTCTATTGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACC 227
                                                                                                                   189 TCCCTGTGGGCATATCTGCTTTAGCCATGCTTTTTGGATCTGGCTCTAGGACC 248
                                                                                                                                                               228 CATGACGAGATTTTAGAAGGTTTAAACTTTAATTTGACCGAAATCCCAGAAGCCCAAATT 287
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49 CCAGTCATCACGACCAAGACCATCCGACTTTTAATAAATTACTCCAAATTTAGCCGAAT 108
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                                                                                                                                                                                                            APPLICANT: Horne, Darci T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTAMES PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M14091
US-09-880-107-2257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 193; DB 10; Length 1872;
49.2%; Pred. No. 2.7e-39;
Live 0; Mismatches 580; Indels 15
                                                                                                                                                  ; Sequence 2257, Application US/09880107; Patent No. US20020142981A1
Matches 576; Conservative
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Best Local Similarity
                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                           US-09-880-107-2257
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APPLICANT: Majumder, Kumud
APPLICANT: Majumder, Kumud
APPLICANT: Spadenra, Steven K.
APPLICANT: Spadenra, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
TITLE REFERENCE: 15966-613
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 1245
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                              706 GCAAAAATTAAGTTCTTGGGTCTTATTAATGAAGTATTTAGGTAACGCTACTGCTATTT 765
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589 ACTGGGAACGTCCTTTCGAGGTTAAAGATACTGAAGA---GGAAGATTTTCATGTTGATC 645
                                                                                       646 AAGTTACTACTGTCAAAGTTCCAATGATGAAAAAAGACTGGGTATGTTCAATATTCAACATT
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ORGANISM: Homo sapiens
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US-09-755-665-13
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                                                                                                                                                                                                  220 CTATCCCCCTTGAGCATCTCTACAGCTTTCTCCATGCTGTGCTGTGGGTGCCCAGGACAGC 279
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                                                                                    105 GAATITGCTITTTCTTTGTATAGACAATTAGCTCATCAAAGTAATTCTACTAACATTTT 164
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12.5%; Score 190.8; DB 10; Length 1245; 49.2%; Pred. No. 8.3e-39;
                                         0; Mismatches 547; Indels
                                                Matches 535; Conservative
    Query Match
Best Local Similarity
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1078 AAGAAGTCTTCTCCACACAGGTGACTGTCTGGGATCACAGGGGATAAGGACCTGATGG 1137
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                                                                403 TAGAAGACGTCAAGAAACTATATCATAGTGAGGCTTTTACCGTTAATTTTGGTGATACTG 462
              478 AGAICAGIACAGGCAAIGCCCTGTTIAITGAAAAACGCCTTCAGGTCCTGGCAGAGTTCC 537
                                                                                                             538 AGGAGAGGCAAAGGCTCTGTACCAAGCTGAGGCCTTCACAGCTGATTTCCAGCAGTCTC 597
                                                                                                                                                                           463 AGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTAAGATCGTTG 522
                                                                                                                                                                                                    523 ACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATTTTTTTCA 582
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; OTHER INFORMATION: Clone ID: 52-LIB34-079-Q1-E1-E8
US-09-960-352-12287
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SEQ ID NO 12287
LENGTH: 391
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US-09-960-352-12287
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1174 CTGCTGATTTACAGCGAGAAAATACCTTCCGTGCTCTTCCTGGGAAGATTGTTAACCCT 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 TCTTCTCCCCACTTAGCATCTCAGCCGCCTTGGCCGTCGTCCCTGGGAGCAAAGGGCA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Genbank Accession No. US20020119462A1 D00753
US-09-917-800A-1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFPLICANT:

TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 4492.5038-02

CURRENT APPLICATION NUMBER: US/09/917,800A

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/222,040

PRIOR FILING DATE: 2000-17-31

PRIOR APPLICATION NUMBER: US 60/222,040

PRIOR FILING DATE: 2000-11-02

PRIOR APPLICATION NUMBER: US 60/290,029

PRIOR FILING DATE: 2001-05-11

PRIOR PRIOR APPLICATION NUMBER: US 60/290,645

PRIOR FILING DATE: 2001-05-15

PRIOR PRIOR DATE: 2001-05-15

PRIOR PRIOR PRIOR DATE: 2001-06-16

PRIOR PLING DATE: 2001-06-19

PRIOR FILING DATE: 2001-06-19

PRIOR FILING DATE: 2001-06-19

PRIOR FILING DATE: 2001-06-19

PRIOR PILING DATE: 2001-07-09

SOFTWARR: PAPELICATION NUMBER: US 60/293,459

PRIOR FILING DATE: 2001-07-09

SOFTWARR: PAPELICATION NUMBER: US 60/303,459

PRIOR FILING DATE: 2001-07-09

SOFTWARR: PAPELICATION NUMBER: US 60/303,459

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PRIOR FILING DATE: 2001-07-09

SOFTWARR: PAPELICATION NUMBER: US 60/303,459

PRIOR FILING DATE: 2001-07-09

SOFTWARR: PAPELICATION NUMBER: US 60/303,459

FROM THE SEQ ID NOS: 1740
                                                                                                                                                                                                                                                                  Sequence 1325, Application US/09917800A Patent No. US20020113462A1 PERERAL INFORMATION:
APPLICANT: Mendrick, Donna
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
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                                                                                                                                 1234 ATTGGAAA 1241
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US-09-917-800A-1325
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Sequence 12287, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICANTON NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 62-LIB34-086-Q1-E1-H6
US-09-960-352-14649
                                                                                                                                                                                                                                      540 GATCGTGATACCGTCTTCGCACTAGTTAACTATTT 576
                                                                                                                                                                                                                                                                       392 GACCCANACACAGITITITGCICTGGIGAATTACATIT 428
                                                                                                                                                                                                                                                                                                                                                              Sequence 14649, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.9%;
Best Local Similarity 58.2%;
Matches 239; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wordbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND FORDESTION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION DOS: 15112
SEQ ID NO 10531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 CAAGAGTIGITGAGAACTITGAATCAACCIGATICTCAATIGCAATTAACTACTAGTAAC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 ATTGCCACTGCTTTCGCCATGTTGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATT 239
                                                                                                                                                                                                                                                                                                                                                                                                                      636 CATGITGATCAAGITACTACTGICAAAGITCCAATGAIGAAAAGACTGGGIATGITCAAT 695
                                                                                                                                                                                                             GATACTGAGGAAGCTAAAAAGCAAATTAATGATTATGTTGAGAAAGGCACCCAGGGTAAG 515
                                                                                                                                                                                                                                                                                516 ATCGTTGACCTAGTTAAAGAATTAGATCGTGATACCGTCTTCGCACTAGTTAACTATATT 575
                                                                                                                                                                                                                                                                                                                 182 ATTGTGGAGTTGGTAAAGGTTCTTGACCCAAACACAGTTTTGCTCTGGTGAATTACATT 241
                                                                                                                                                                                                                                                                                                                                                   576 ITITICAAGGGIAAGIGGGAACGICCTITCGAGGITAAAGAIACIGAAGAGGAAGAITIT 635
                                                                                                                                                                                                                                                                                                                                                                              32 ATTGCTTCAGCCTTTGCTATGCTCTCCCTGGGAGCCAAGGGCAACACTCACACTGAGATC 91
                                                                     336 CAATTGCAATTAACTACTGGTAACGGTTTATTTTTGTCTGAAGGTTTAAAATTGGTTGAC 395
                                                                                                                                        396 AAATTCCTAGAAGACGTCAAGAAACTATATCATAGTGAGGCTTTTACCGTTAATTTTGGT 455
                                                                                                                                                            0; Gaps
                                       Gaps
                                                                                                     2 CAGCTGCAACTGACCACTGCCAATGGTCTTCATCAATGAGAGTGCAAAGCTAGTGGAT 61
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Pred. No. 8.8e-28;
0; Mismatches 157; Indels 0;
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Score 161; DB 10; Length 391;
Pred. No. 1.7e-31;
                                       Indels
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OTHER INFORMATION: Clone ID: 45-LIB34-014-Q1-E1-D2
                                         0; Mismatches 135;
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Best Local Similarity 60.5%;
         10.6%;
64.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 CTCCACTACTGCGACAA 378
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                                       Matches 242; Conservative
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            Query Match
Best Local Similarity
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APPLICANT: Warrense, Wesley C.
APPLICANT: Tao, Nongbing
APPLICANT: Tao, Nongbing
APPLICANT: Tao, Nongbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 icrecciedeaeccaagecaacacreacacreagarecreaaegecreggrircaace 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 IGACCGAAAICCCAGAAGCCCCAAAIICACGAGGGIIITCAAGAGIIGIIGAGAACIIIGA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 ATCAACCTGATTCTCAATTGCAATTAACTACTGGTAACGGTTTATTTTTGTCTGAAGGTT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 TGAGTTTAGGTACTAAAGCCGATACCCATGACGAGATTTTAGAAGGTTTAAACTTTAATT 261
                                                      360 GGTTTATTTTGTCTGAAGGTTTAAAATTGGTTGACAAATTCCTAGAAGACGTCAAGAAA 419
                                                                                     420 CIATATCATAGTGAGGCTTTTACCGTTAATTTTGGTGATACTGAGGAAGCTAAAAAGCAA 479
                                                                                                                                                                                                                   272 crgrarcacrecgaagcerrerecarcaacrreaggargergaggaggecaagaagaag 331
                                                                                                                                                                                                                                                                            480 ATTAATGATTATGTTGAGAAAGGCACCCAGGGTAAGATCGTTGACCTAGTTAAAGAATTA 539
                                                                                                                                                                                                                                                                                                        Gaps
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152 CAGCATCTICTCCACCACCCTGAACCAACCAACCACCAGCTGCAACTGACCACTGGCAAT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 AAAGTAATTCTACTAACATTTTTTTAGTCCTGTTTCTATTGCCACTGCTTTCGCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 172; Indels
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Search completed: December 7, 2002, 02:10:11 Job time : 60 secs

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